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FIG. 1

Human NRSF Amino Acid Sequence

MATQVMGSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAP  
QLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVGDNNFSDSEEGLEESADIKGE  
PHGLENMELRSLLELVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAEESEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRC  
DRCGYNTNRYDHYTAHLKHHTRAGDNERVYKCICTYTTVSEYHWRKHRLRNHFPRKVY  
TCGKCNFYSDRKNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFC  
DQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCP  
VCDYAASKKCNLQYHFKSKHPTCPNK TMDVSKVKLKKTKKREADLPDNITNEKTEIEQ  
TKIKGDVAGKKNEKSVKAEKRDVSKKEKPSNNVSVIQVTRTRKSVTEVKEMDVHTGS  
NSEKFSKTKKSKRKLVDHSLHGPVNDEESTK KKKVESKSKNNSQEVPKGDSKVE  
ENKKQNTCMKKSTKKTLKNKSSKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKG  
PVQVELPPPMEHAQMEGAQIRPAPDEPVQMEVVQEGPAQKELLPVVEPAQMVG AQIVL  
AHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAPMQVVQKEPVQMELSPPMEVV  
QKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPP  
PPREPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVS  
TEDLSPSPPLPKENLREEASGDQKLLNTGEGNKEAPLQKVGAEEADESLPGLAANIN  
ESTHSSSGQNLNTPGETLNGKHQTDIVCEMKMDTDQNTRENLTGINSTVEEPVSP  
MLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGHSGHSDLSDNMSEGSDDS  
GLHGARPVPQESSRKNKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVY LEEAAQGGQE

1050 682.4 5011610 31 068 5002

## FIG. 2

## Human NRSF cDNA sequence

1 ggcggcggcg gcggcgccga ctgggtgcgc ggcgccagcgt cctgtgttgg aatgtgcggc 61 tgcgcggagc tgcggcgga gcaagcggga gcaagcggcg ggcggcgacc 121  
 ctggcgccgc ctggcgagc cgaagacggca gggcgagggc cggcgagggc ttctgggccc tctgggtcca cgaagggccc agcaccaca ttaccacc 241 tccccacct  
 ctccccga actccagca caaagaaaaa tggcggga tggcggggc 301 actcgggtc gcccggccc cctcacggag gaagggcggaa tacagtatg gccaccaggg 361 taatggggga gttcttgg  
 ggaaggggc tgtttaccag cagtggaac attgggaatg 421 cccggccta cgaatgtat gactgtcatg accttccaa agctgaatg gccggacctc 481 agcttaatt gctggcgaat gttggcctaa  
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 catatcgta 1321 ctatcagg tgaagggca acttaaaa atcagtgcag ttatgtggc ttaataac 1441 atgaagttaac ccggcatgca agcaggtc tcaagttc agaagacta tctaacta  
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 aaaacttga 2101 aaaaatac agttaagaaa agcagttaa gttcagaa ggaacctgt gagaagggat 2281 ggccgtgtcc tgaagagctt gttcagatgg aggtgtgttca ggagggggcct gttcagaagg 2341  
 2221 ccgtttagt ggaagctgcca cttccatgg agcatgtca gatgtgaggg gttcagatag 2401 tggagctgccc tcttccatg ggaagggaggt tgcacaaatg ggccctgtc 2461 ccatgggaac  
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 gaacaaagggt 3661 tca

## Mouse NR5F Amino Acid Sequence

MATQVMGQSSGSLFNNSANMGMALTNDMYDLHELSKAELAAP.  
QLIMLANVALTGEASGCCDYLVGEERQMAELMPVGDNHFSEGEGLSEADLKGLE  
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NYFSDRKNNYVQHVTRHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKFPCDQCNY  
VASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCVP CDYA  
ASKKCNLQYHFKSKHPTCPSKRMDVSKVKLKKTKKREADLLNNAVSNKEMENEQTKTK  
GDVSGKKNEKPVKAVGKDA SKEKKPGSSVVQVSTRTRKSAAETKAAEVKHTDGO  
TGNNPEKPKAKKNKRKKDAEAHPSEEPVNEGVP TKKKKSECKSKISTNVPKGGGRA  
EERPGVKKQSASLKKGTNKTTPPKTKTSKKGKGLAPKGMGTQTEPSSGALAQVGVSPDPA  
LIQAEVTGSGSSQTELPSPMDIAKSEPAQMEVSLTGPPPVPEPAQMEPSPAKPPQVEAP  
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EELPQAEPPPMEDCQKELPSVPEAQIEVAQTAPTQVQEEPPPVSEPPRVKPTKRSSL  
RKDRAEKELSLSEMARQEQVLMGVGLVPVRDSKLLKGNKSAQDPPAPPSPKGNR  
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ASHSKCQTGSSGLCDVDTEQKTDTPMKD SAAEPVSPPTPTVDRDAGSPAVVASPPT  
LAENESQDEIDEGIHSHDGS DLSDNMSEGSDDSLGHGARTPPEATSKNGKAGLAGK  
VTEGEFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEAAEEQEEQEEEREEQE

## Mouse NRSF cDNA

[illegible]

**FIG. 5**  
**Rat NRSF Amino Acid Sequence**

MATQVMGSSGGSLFNNSGNMGMALPNDMYDLHDLSKAELAAP  
 QLIMLANVALTGEVNGSCCDYL VGEERQMAELMPV GDNHFSDEGEGLAESAEELKGD  
 SGLDNMELRSLELSVVEPQVFEASAAPEVYSSNKDPAPEAPVAEDKCKNLKAKPFR  
 KPCQYEAEESEEQFVHHIRVHSACKFFVEESAEEKQAKARESGASPEEGEFSGPIRCD  
 RCGYNTNRYDHYTAHLKHLRAGDNERVYKCICTYTTVSEYHWRKHLRNHFRKVVY  
 CSKCNFYFSTEKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCD  
 QCNYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPV  
 CDYAASKKCNLQYHFKSKHPTCPSKTMDSKVKLKTKRREADLHRDAAAAATEQIDT  
 EQAKTKGVDA SARSRERPVKGVGKDVPEKKPCSNASVVQVTRTRKSAVETKAAEGK  
 HTDGGTGNNAEKSSKAKSKRKMDAEAHPSVEPVTEGPTTKKKKTESKPKTSGEVPGK  
 SRVEDRKADKQASIKKGGKKTALKTAKKSKLAPK WVGHTEPSEMAQGESPV  
 PALTQAVVTPSGSTQTELSSPMDIAQTEPAQMDVSQTGPPVQVRPLPVEPAQLEPSPP  
 QEPPQVEPPACVEPPPPVEPPCPMEPAEMEPSPPMEPSQVEPPPHLEPPLMELPQVE  
 LPVEDCCQKELPPVEHAQTKVAQTGPTQVGAVQEEPLFCLRATSSQANQKVISPKDRA  
 KEKLSVLSEMARQEQVLIIEVGLVPVRDSQLLKASKSAPDLPA PPSPLPKGHLRREETP  
 KDQEMFSDGEGNKVSPLEKGGTEEA GESRAELAAPMESTSAL SSEQSSNAPDGETLHS  
 ECQADSTAVCEMEVDTEQKTD RVP LKDSAVEPVSPLNPRVDPEAAAPA VVASPPITLA  
 ESQEIDEDEGIHSHDGS DLSDNMSEGSDSDSLGHGARPAPQEATSKSGEGLAVKVTEG  
 EFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEEAAEEQ

## FIG. 6

### Rat NRSF cDNA Sequence

atgagccacc aggtgtatgagg gcatgtttt ggaaggagagaa gtctctttaa caacagtggc 61 aacatggggca tggccttaac caacgacatg tatgacttc acgaccttc gaaagctgaa 121  
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atttggtaa tgtgtactc 3181 ctgaaagaa cagctgagga gcaagagtag agtagctgat cctcggagg aagcggcaatg 3241 cgatttcta a

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**FIG. 7**  
**Xenopus NRSF partial Amino Acid Sequence**

MATQMVNQSTGNSLFCSTSTYSNISLDNDMYGLHDLISKADMAAPR  
LIMLANVALTGELSSGCCDYTPGERQMAELTTVNDNSFSDSEGDRLSDPSMDIQSH  
NFIMEMEPAECSKEGTSENDGTLISNTLEVEVQDKRTPSPTDDKYKCVKSKPFRCKP  
CQYKAESEEEFVHHIKIHS AKIYVDNDSNKKAQGNEADSSISESDVSKGPIQCDCRG  
YNTNRFHDHYLAHLKHHNKAGENERVYKCTICTYTTVSEYHWKKHLRNHYPRILYTCSQ  
CSYFSDRKNNYIQHIRTHTGERPYQCILCPYSSSQKTHLTRHMRTHSGEKPFKCEQCS  
YVASNQHEVTRHARQVHNGPKPLTCPHCDYKTADRSNFKKHVELHVNPRQFLCPVCDY  
AASKKCNLQYHIKSRHSGCTNITMDVSKVKLRTKKGDIGVADV DANKQTENGNIIDKS  
VEETVKAEKRESCGKAKKSIVNLVDGQVAKRRRLSSTQKKKTS DARPEKILDKSRKS  
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FIG. 8

## Xenopus NRSF partial cDNA sequence

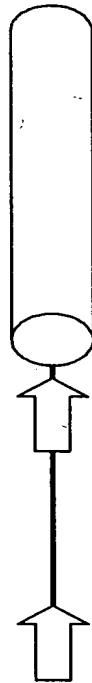
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121  tggtaacca gtctacaggt aacagcttgt tctgtaccag cacctactcc aatatttcac
181  tggacaatga catgtatggg ttgcataacc ttcaaaaagc tgatatggca gccctcgat
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661  ataatgactc aaataaaaaa gcgcagggtg atgaggcaga ttctagcata tcggagggaat
721  ctgatgtctc caaaggacct attcagtggt acaggtgtgg atacaataga aatcgttttg
781  atcactatct ggctcattta aagcatcaca acaaaagctg agaaaaatgaa agagtataca
841  aatgtacaat atgtacttat actacagtca gtgaatatca ctggaagaaa catctacgtc
901  accattatcc aaggatactc tatacatgct cacaatgttc ctatttttct gataggaaaa
961  ataattatat ccagcatata agaacacata caggagaacg accatatcag tgtattctat
1021  gtccttactc aagctcacag aaacccact tgaccaggca catgcgaact cattcaggtg
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1561  catctactca gaaaaaaatt aaaacttcag acgcaaggcc tgaaaagatt ttagataaat
1621  cccgtaagtc tagttgtgtg aaagaaaaat ctgatttatt agaaaattct aatgataccc
1681  aaacaagcac tgtg

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1990



NRSF	KPFR	CKP	--	CQY	EAE	SEEQFVH	<u>H</u>	IRV	-	HS	AKKFFVEESA	EKQAKARE	SGSSTA	EEGDF	SKGP
	IR	CDR	--	CGY	NTN	RYDHYTA	<u>H</u>	HLKH	-	H	TRAGD	NERV			
	YK	CII	--	CTY	TTV	SEYHWRK	<u>H</u>	HLRN	-	H	FPRKV				
	YT	CGK	--	CNY	FSD	RKNNYVQ	<u>H</u>	VRT	-	H	TGERP				
	YK	CEL	--	CPY	SSS	QKTHLTR	<u>H</u>	MRT	-	H	SGEKP				
	FK	CDQ	--	CSY	VAS	NQHEVTR	<u>H</u>	ARQV		H	NGPKP				
	LN	CPH	--	CDY	KTA	DRSNFKK	<u>H</u>	VEL	-	H	VNPRQ				
	FN	CPV	--	CDY	AAS	KKCNLQY	<u>H</u>	FKSK		H	PTCPN				

FIG. 10

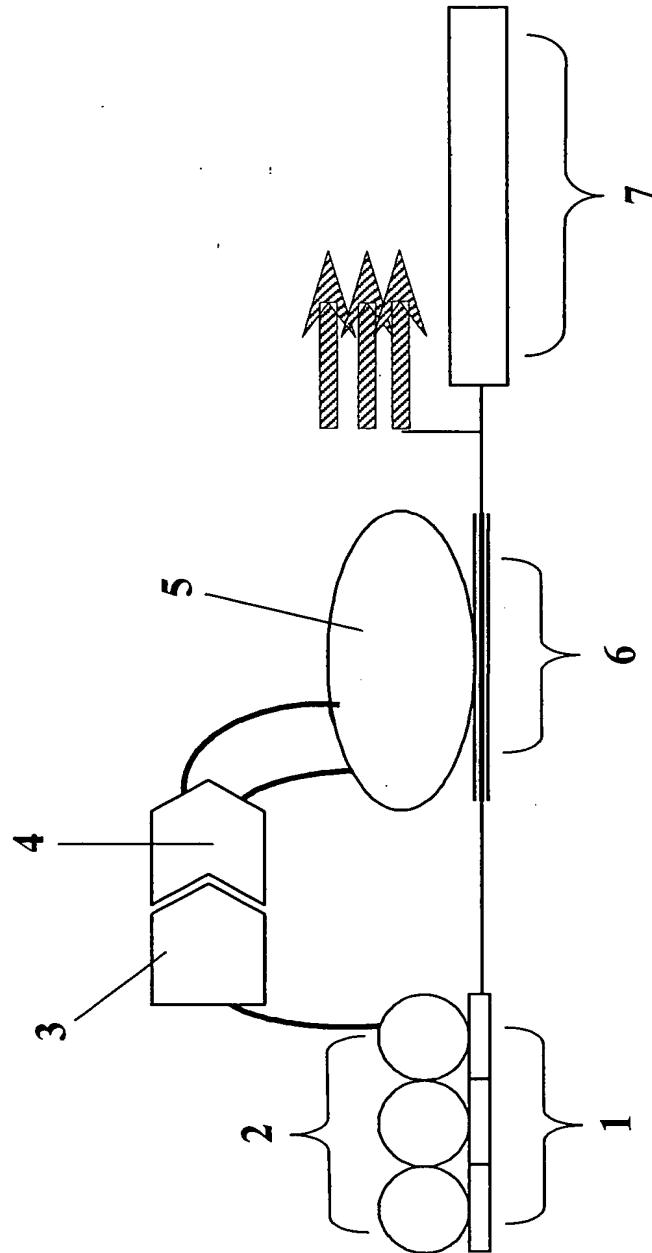


FIG. 11

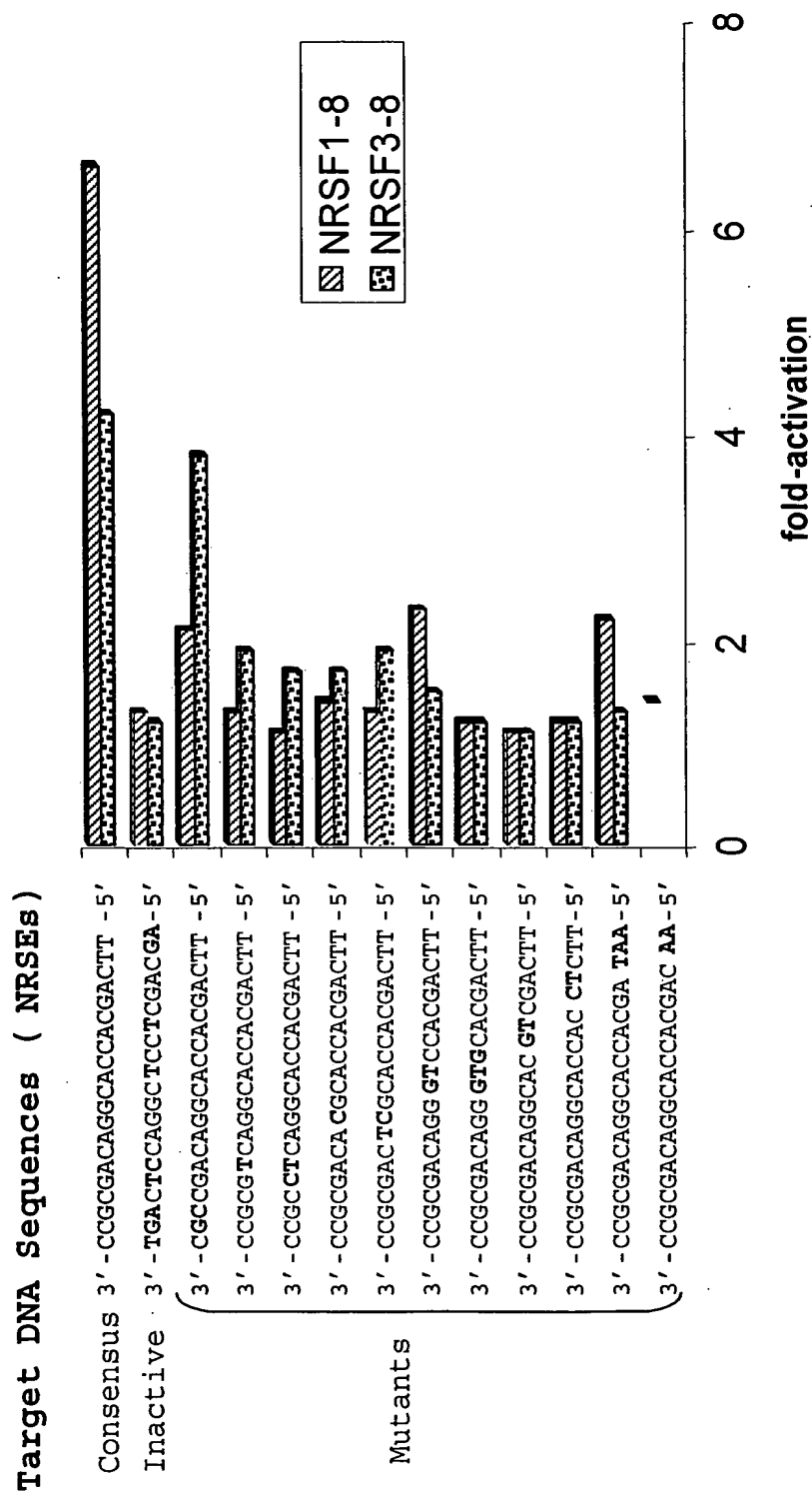


FIG. 12

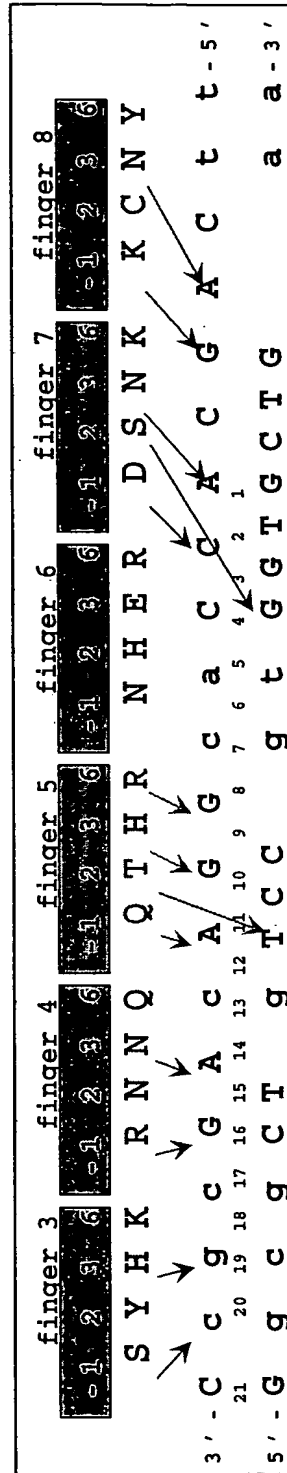


FIG. 13

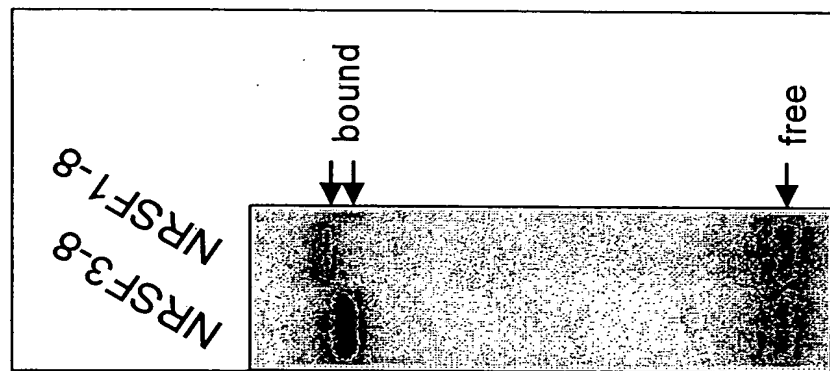


FIG. 14

A. Finger 4 Selections		B. Finger 5 Selections	
3'-CCGCC <u>TC</u> AGGCACGACTT-5'		3'-CCGCGACT <u>TC</u> GACACGACTT-5'	
-1	1 2 3 5 6	-1	1 2 3 5 6
NRSF F4v1	H K T R M E	NRSF F5v1	T V G T R R
NRSF F4v2	H K T R M E	NRSF F5v2	T R G T K R
NRSF F4v3	H K T R M E	NRSF F5v3	T G S T R R
➔ NRSF F4v4	H R T R M E	➔ NRSF F5v4	T M S G R R
NRSF F4v5	H K T R K E	NRSF F5v5	T I S A R R
NRSF F4v6	H L T R K E	➔ NRSF F5v6	H M P T R R
NRSF F4v7	H K T R A E	NRSF F5v7	H R G T V R
➔ NRSF F4v8	H K T R D E	NRSF F5v8	R A P D K R

FIG. 15A

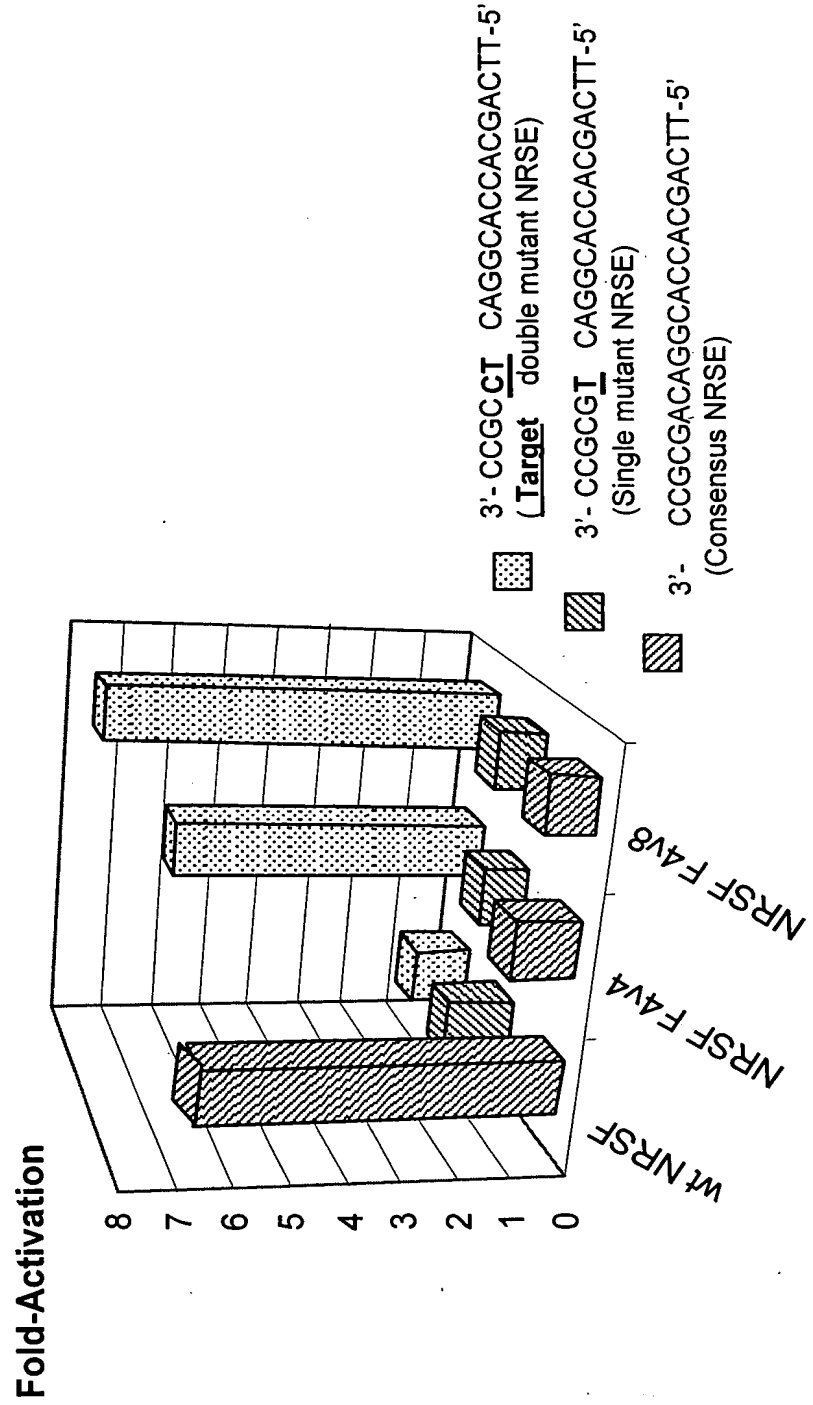


FIG. 15B

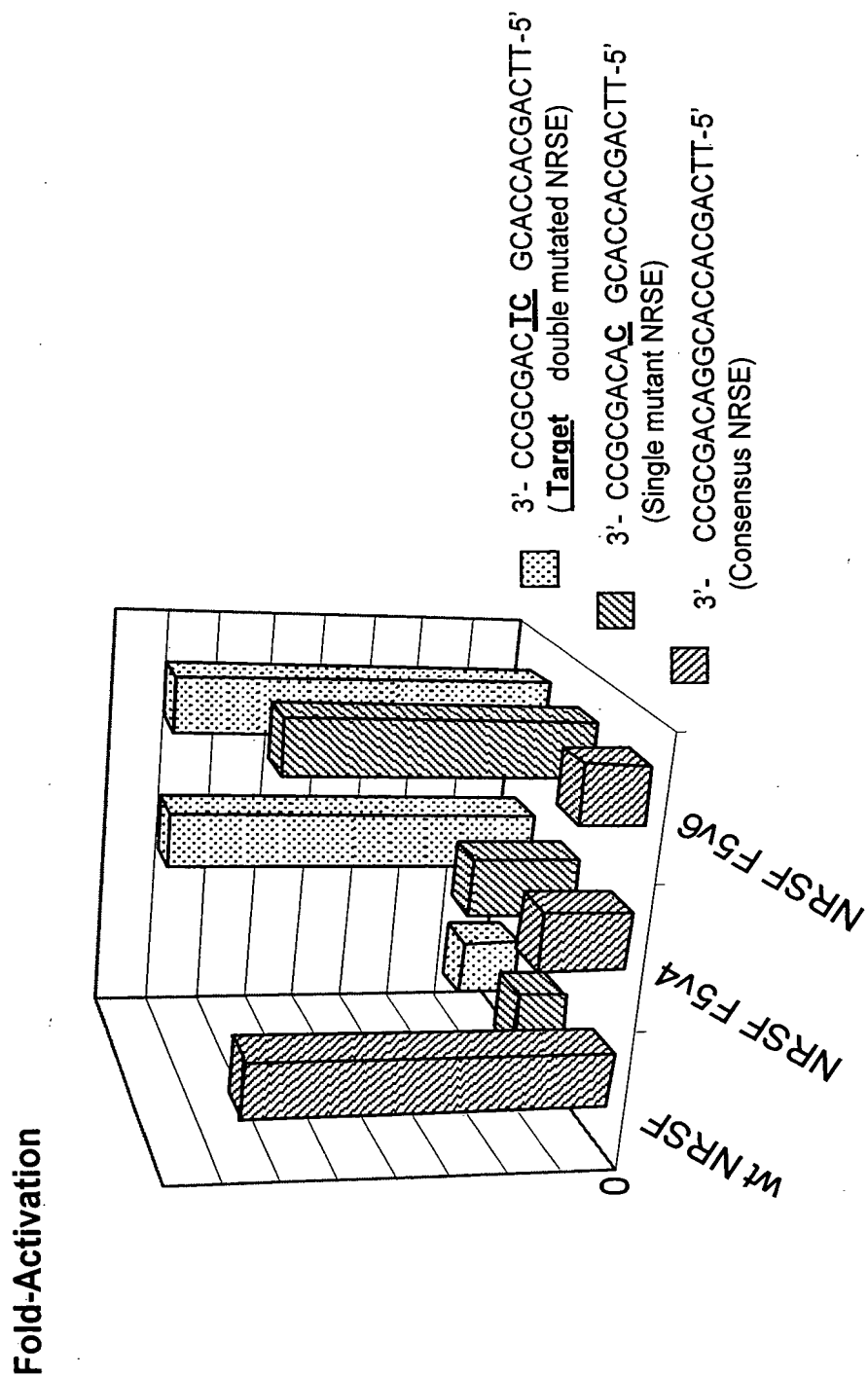
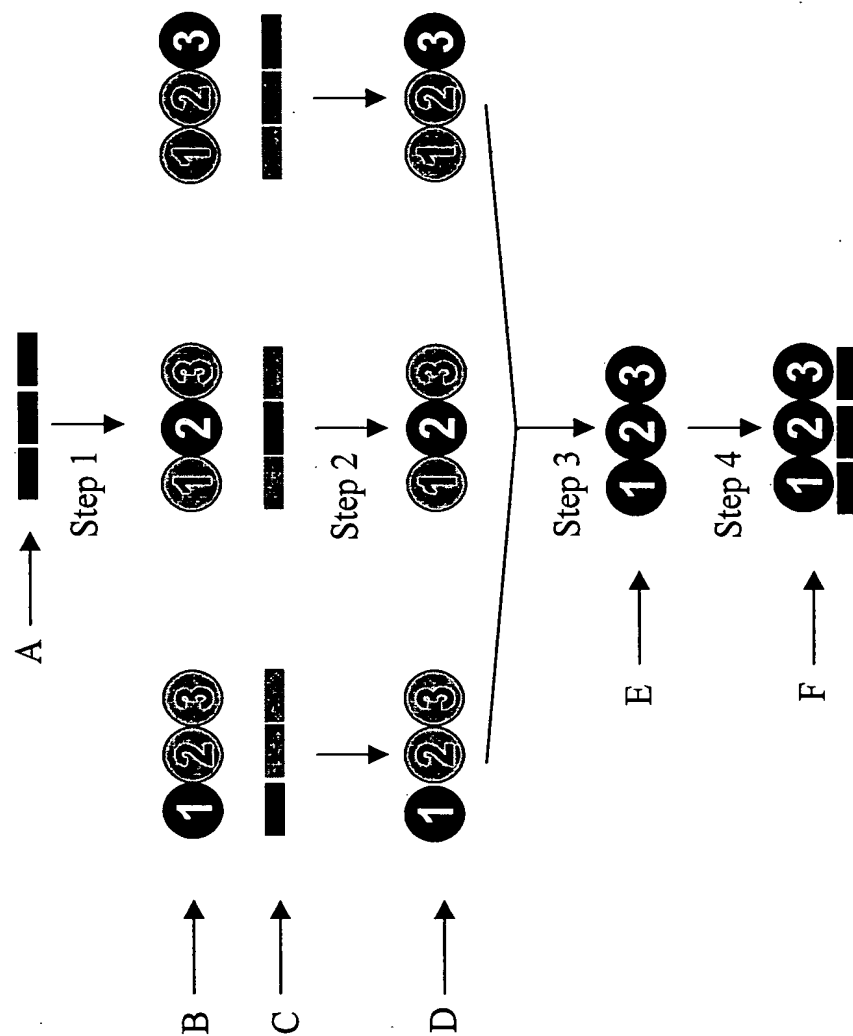




FIG. 16



10/532031

FIG. 17

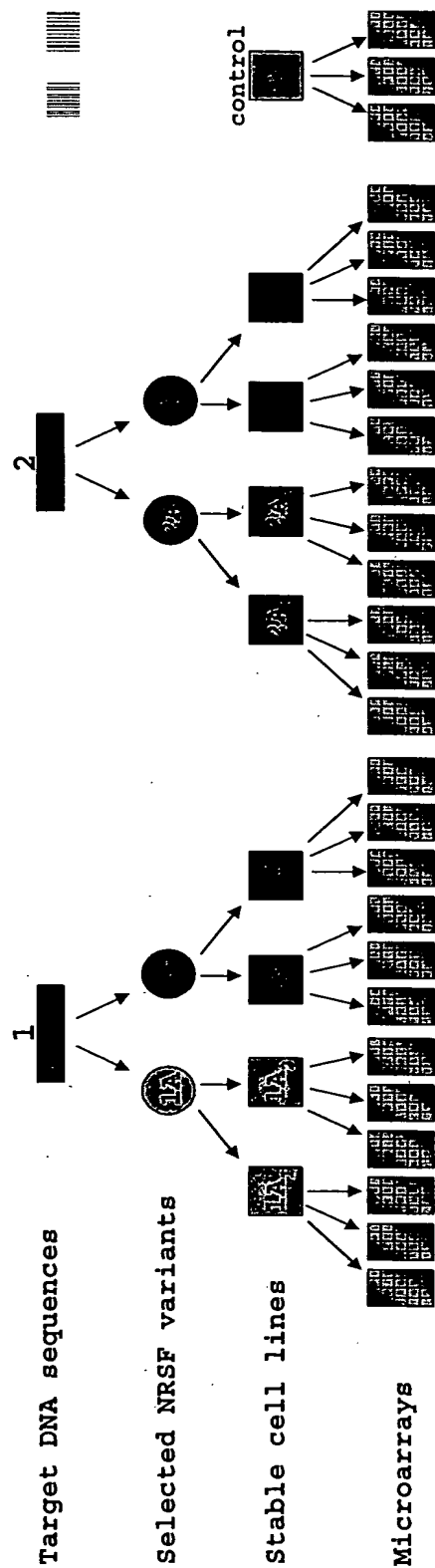
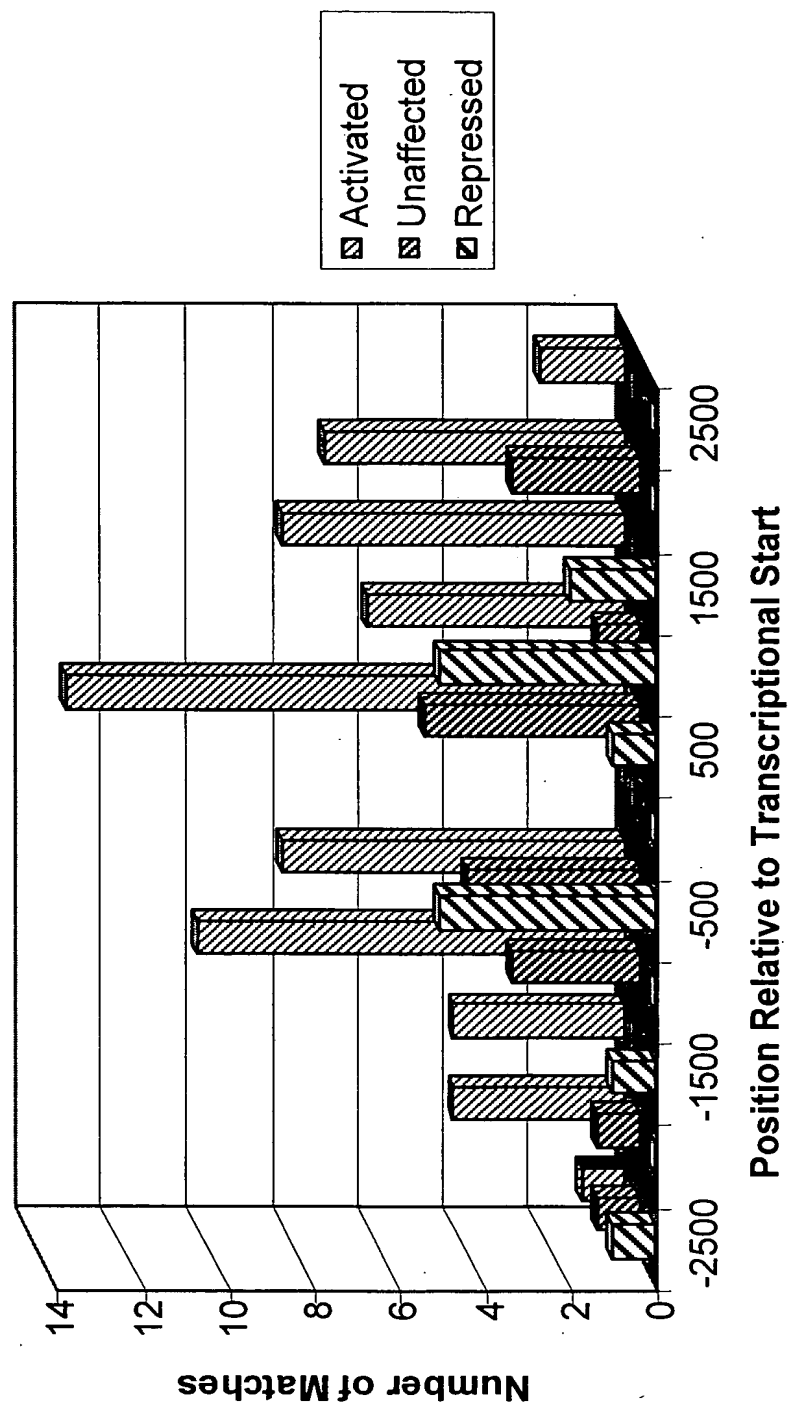


FIG. 18



## FIG. 19

F4v1 (sequence identical to F4v2, F4v3)

MATQVMGSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGEGLEESADIKGEPHGLENNMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESAEEKQAARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYSD**HKTRY**MEHVTRHTGERPYKCELCPYSSSQKTHLT  
RHMRTSHGKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKKREADLPDNI<sup>1</sup>TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL<sup>2</sup>EVDSHSLHGPVNDEESSTK<sup>3</sup>KKKKVSKSKNNSQ<sup>4</sup>EVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKGSQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME<sup>5</sup>LPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPEVVQKEPVQME<sup>6</sup>LSPPMGVVQKEPAQREPPPP  
REPLHMEPI<sup>7</sup>SKKPPLRKDKKESNMQSERARKEQV<sup>8</sup>LIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINETHISSGQNLNTPEGETLNGKHQTD<sup>9</sup>SIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQ<sup>10</sup>EIDEDEGIHSHGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCI<sup>11</sup>FCDRSFRKGDYSKHLNRHLVNVYYLEEAAQGE

FIG. 20

F4v4

MATQVMGQSSGGGLFTSSGNIGMALPNMDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEEQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENMELRLELSVVEPQPVFEASGAPDIYSSNKDLPPEPTPGAEDKGSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCNFYFSDHRTRYMEHVTRHTGERPYKCELCPYSSSQKTHLT  
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLTKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKPKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKSKRKLEVDSHSLHGPVNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKQSAQMDPPQMGPAQTEAVQKGPVQVELPPMEHAQME  
GAQIRPAPDEPVQMEVVEGPAQKELLPPVEPAQMVGAQIVLAHMELPFPPMETAQTEVAQMGPAQMEPAQMEVAQVESAP  
MQVVQKEPVQMEVVEVQKEPVQIEVQKEPVQKEPVQIEVQKEPVQKEPVQIEVQKEPVQKEPVQKEPVQKEPVQKEPVQ  
REPPLHMEPI SKKPPPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINESHISSSGQNLNTPEGETINGKHQTDI VCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLNVVYYLEEAAQGGQE

FIG. 21

F4v5

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGEGLEESADIKGEPHGLENNMELRSLSELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYSFSDHKTRYKEHVTHTGERPYKCELCPYSSSQKTHLT  
RHMRTSGEKPFPKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKKPS  
NNVSVIQVTTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSHSLHGPVNDDEESTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPTEAVQKGPVQVELPPMEHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPMETAQTEVAQMGPAPEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEAEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIIDEDEGIHSHGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGFVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEAAQGE

FIG. 22

F4V6

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLKAEALAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESAEEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCNYSFSDHLTRYKEHVTRHTGERPYKCELCPIYSSSQKTHLT  
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAAASK  
KCNLQYHFKSKHPTCPNKTMDSVKVCLKTKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKPKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSHGHGPNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKGSQMDPPQMGPPAPTEAVQKGPVQVELPPMEHAQME  
GAQIRPAPDEPVQMEVVEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMVEVVQKEPVQIELSPPMVEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLINGKHQTDTSIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVYYLEEAAQGGQ

FIG. 23

F4v7

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGGLEESADIKGEPHGLENNMELRSLSVVEPQPVFEASGAPDIYSSNKDLPPEPTGAEDKGKSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESAEEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCNYFSD**HKTRYAE**HVTRHTGERPYKCELCPYSSSQKTHLT  
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKKTADRSNFKKHVELHVNPRQFNCPCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKPKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSSHGHGPNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPEAVQKGPVQVELPPMEHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPISSKKPPLRKDKKEKSNMQSERARKEQVLIIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLNTGEGNKEAPLQKVGAEEADESLPGLAANINESHISSSGQNLNTPEGETLNGKHQTDISIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNYYYLEEAAQGE



## FIG. 24

F4v8

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSLLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRVDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYSFSDHKTTRYDEHVTRHTGERPYKCELCYSSSSQKTHLT  
RHMRTSHSGEKFCKDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTAADRSNFKKHVELHVNPRQFNCPCVDYAASK  
KCNLQYHFKSKHPTCPNKTMDSVKVKKLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESTKTKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGSQAQMDPPQMGPAFTEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVQEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPMETAQTEVAQMGPAPEPAQMEVAQVESAP  
MQVVQKEPVQMELESPPMEEVQKEPVQIELESPPMEEVQKEPVQIEVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLEI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPGETLNGKHQTDIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHGEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDVFVCI FCDRSFRKGDYSKHLNRHLVNVYILEEAAQGE

FIG. 25

F5V1

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSEL SVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHS AKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFFPRKVYTCGKCN YFSDDRKNNYVQHVRTHHTGERPYKCELCPYSSSTVGTLLR  
RHMRTSHGKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVC DYAAASK  
KCNLQYHF KSKHPTCPNK TMDVSKVKL KTKK READLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVD SHSLHGPVNDEESSTK KKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVVEGPAQKELLPPVEPAQMVGAI VL AHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPLRLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINES THISSGQNLTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVYLEEAAQGE

FIG. 26

F5v2

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEEQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSLSVPEQPVFEEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHSACKFFVEESAEEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICITYTTVSEYHWRKHLRNHFFPRKVYTCGKCNYSFSDRKNNYVQHVTRHTGERPYKCELCPYSSSTRGTLK  
RHMRTSHGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDSEESTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVVEGPAQKELLPPVEPAQMVGAIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMVVEVQKEPVQIELSPPMVVEVQKEPVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKESNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESITHISSGQNLNTPEGETLNGKHQTDIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEAAQGE

FIG. 27

F5v3

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAE LAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENMELRSLSEL SVVEPQVFEEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAESÉEQQFVHHIRVHSAKFFVEESA EKQAKARESGSSSTAEEGDFSKGPIRCDCRGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYSFSDRKNNYVQHVRTHTGERPYKCELCPYSSSTGSTLR  
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTA DRSNFKKHVELHVNPRQFNCPVC DYAAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNI TNKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL EVD SHLHGPVNDEESSTK KKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKTLLKNKSSKSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEV VQEGPAQKELLPPVEPAQMVG AQIVLAH MELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPM EVVQKEPVVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPGETLNGKHQTD SIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGD FVCIFCDRSFRKGDYSKHLNRHLVNVYYLEEA AQQE

## FIG. 28

F5v4

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGSSKTKPFR  
CKPCQYEAEEQFVHHIRVHSAKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRDYHTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFRKVVYTCGKCNYSFDRKNNYVQHVTRHTGERPYKCELCPYSSSTMSGRLR  
RHMRTSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTAADRSNFKKHVELHVNPRQFNCPCVDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELEPPPMETAQTEVAQMGPAPEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKESNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDI VCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAQGE

FIG. 29

F5v5

MATQVMQSSGGGLFTSSGNI GMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSL ELSVVEPQPVFEASGAPDIYSSNKDLP PETPGAEDKGKSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHSAKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFP RKVYTCGKCNYSFSDRKNNYVQHV RTHTGERPYKCELCPYSSSTISALR  
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVC DYAAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLLKTKK READLPDNI TNEKTEIEQTKIKGDVAGKNEKSVKAEKRDVSKKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGNSSEKFSKTKKSKRKLEVD SHSLHGPVNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPM EHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAH MELPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMMEVVQKEPVQIELSPPMMEVVQKEPVQIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEEADESLPGLAANIN ESTHISSSGQNLTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCI FCDRSFRKGDYSKHLNRHLVNVYYLEEAAQOQE

## FIG. 30

F5v6

MATQVMGQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG  
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLSELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAESSEEQFVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNFYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSHMPTLR  
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPCVCDYAASK  
KCNLQYHFKSKHPTCPNKTMDSVKVCLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKKPS  
NNVSVIQVTTTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKL EVDSHSLHGPVNDEESSTK KKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSQAQMDPPQMGPAPTEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVQEGPAQKELLPPVEPAQMVGAI VLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPPMEEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPPLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVLI EVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLLNTGEGNKEAPLQKVGAEAEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDTSIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGD FVCIFCDRSFRKGKDYSKHLNRHLNVVYYLEEAAQQQE

## FIG. 31

F5v7

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYL VGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENNMELRSLSVPEQPVFEEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESAQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYSFSDRKNNYVQHVRTHTGTERPYKCELCPYSSSS**HRGTLV**  
RHMRTSGEKPFFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTAADRSNFKKHVELHVNPRQFNCPCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVD SHSLHGPVNDEESSTK KKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGSQAQMDPPQMGPA TEAVQKGPVQVELPPPMHAQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHME LPPMETAQTEVAQMGPAPEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMELSPPEVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQKEPVQ  
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQV LIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT  
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVYILEEAAQQGE



**FIG. 32**

F5v8

MATQVMQSSGGGLFTSSGNIGMALPNDMYDLHDL SKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG  
DNNFSDSEEGELEESADIKGEPHGLENMELRSLSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR  
CKPCQYEAEESEEQFVHHIRVHSAKKFFVEESA EKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR  
AGDNERVYKCI ICTYTTVSEYHWRKHLRNHFPRKVYTCGKCN YFSDRKNNYVQHVTRHTGERPYKCELCPYSSSRAPDLK  
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTA DRSNFKKHVELHVNPRQFNCPCVCDYAASK  
KCNLQYHFKSKHPTCPNKTMDVSKVKLTKTKKREADLPDNIITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKKKPS  
NNVSVIQVTRTRKSVTEVKEMDVHTGSNSEKFSKTKSKRKLEVD SHSLHGPVNDEESSTKKKKVESKSKNNSQEVPK  
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKSSKPPQKEPVEKGS AQMDPPQMGPAPTEAVQKGPVQVELPPPMEH AQME  
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQI VLAHME LPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP  
MQVVQKEPVQMELSPPMEEVVQKEPVQIELSPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP  
REPLLHMEPI SKKPPLRKDKKEKSNMQSERARKEQVL IEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ  
KLINTGEGNKEAPLQKVGAEEADESLPGLAANINESTHIS SSGQNLTPEGETLNGKHQTD SIVCEMKMDTDQNTRENLT  
GINSTVEEPPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEI DEDEGIHSHEGSDLSDNMSEGSDDSLGHGARVPVQ  
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGDYSKHLNRHLVNVVYYLEEAAQGGQE

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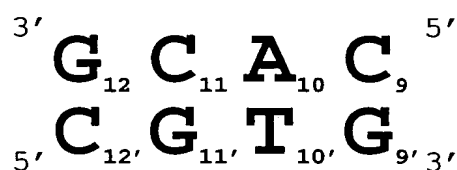
FIG. 33

A.

wild-type F6

-112356

NQHETR

relevant portion  
of NRSE

B.

F6 variants/  
base 9

-112356

DRGNRR

DRGNNR

DKANAR

DLSNRR

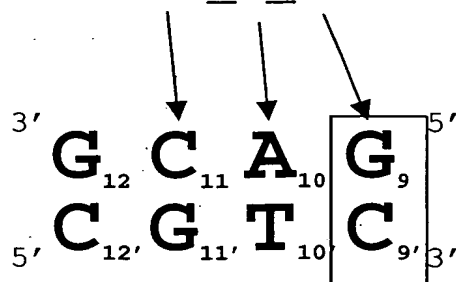
DSTNKR

ERGNQR

ERYAVR

EKYKVI

D+\_N\_R

F6 variants/  
base 11

-112356

RREREL

RREKVM

RRERYI

RRDNET

RRDGAN

RKDLAL

RADIRL

RLELKV

RRD

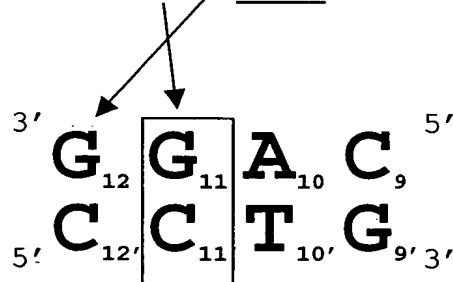
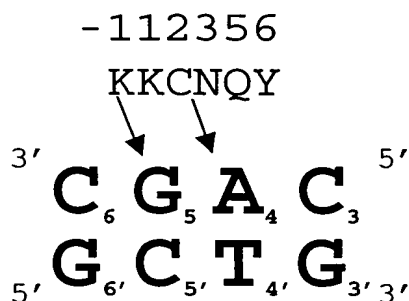


FIG. 34

A.

wild-type F8

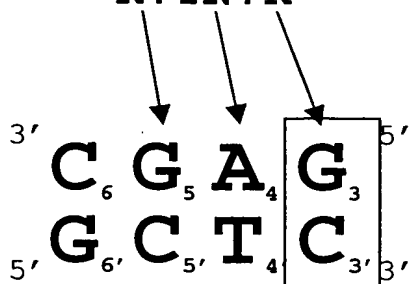
relevant portion  
of NRSE



B.

F8 variants/  
base 3

-112356  
RLFNRR  
KKYNRR  
RQYNQR  
TKFNHR  
RKYNRR  
RKYNRR  
RRANVR  
RFYNRR  
R+YN+R



F8 variants/  
base 4

-112356  
RRSTRY  
RRSTRY\*  
RRSTRY\*  
RKATDY  
RRTTLY  
RKATMY  
RRSTQY  
RRSTVY  
R+sT\_Y

